

TITLE: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
Inventors: Ralf M. Luche et al. Docket No. 200125.433
EXPRESS MAIL NO. EL 897872305US

Figure 1

1 CCGGTGCCAG CCCAGGTGCT CGCGGCCTGG CTCCATGGCC CTGGTCACAG TGAGCCGTTT
61 GCGGGCGGGC AGCGGCGCCT CCACGCCCGT GGGGCCCTGG GACCAGGCGG TCCAGCGAAG
121 GAGTCGACTC CAGCGAAGGC AGAGCTTTGC GGTGCTCCGT GGGGCTGTCC TGGGACTGCA
181 GGATGGAGGG GACAATGATG ATGCAGCAGA GGCCAGTTCT GAGCCAACAG AGAAGGCCCC
241 GAGTGAGGAG GAGCTCCACG GGGACCAGAC AGACTTCGGG CAAGGATCCC AGAGTCCCCA
301 GAAGCAGGAG GAGCAGAGGC AGCACCTGCA CCTCATGGTA CAGCTGCTGA GGCCGCAGGA
361 TGACATCCGC CTGGCAGCCC AGCTGGAGGC ACCCCGGCCT CCCCAGCTCC GCTACCTGCT
421 GGTAGTTTCT ACACGAGAAG GAGAAGGTCT GAGCCAGGAT GAGACGGTCC TCCTGGGCGT
481 GGATTTCCCT GACAGCAGCT CCCCAGCTG CACCCTGGGC CTGGTCTTGC CCCTCTGGAG
541 TGACACCCAG GTGTACTTAG ATGGAGACGG GGGCTTCAGC GTGACGTCTG GTGGGCAAAG
601 CCGGATCTTC AAGCCCATCT CCATCCAGAC CATGTGGGCC AACTCCAGG TATTGCACCA
661 AGCATGTGAG GCAGCTCTAG GCAGCGGCCT TGTACCGGGT GGCAGTGCCC TCACCTGGGC
721 CAGCCACTAC CAGGAGAGAC TGAACTCCGA ACAGAGCTGC CTCAATGAGT GGACGGCTAT
781 GGCCGACCTG GAGTCTCTGC GGCCTCCCAG CGCCGAGCCT GGCGGGTCCCT CAGAACAGGA
841 GCAGATGGAG CAGGCGATCC GTGCTGAGCT GTGGAAAGTG TTGGATGTCA GTGACCTGGA
901 GAGTGTCACT TCCAAAGAGA TCCGCCAGGC TCTGGAGCTG CGCCTGGGGC TCCCCCTCCA
961 GCAGTACCGT GACTTCATCG ACAACCAGAT GCTGCTGCTG GTGGCACAGC GGGACCGAGC
1021 CTCCCGCATC TTCCCCCACC TCTACCTGGG CTCAGAGTGG AACGCAGCAA ACCTGGAGGA
1081 GCTGCAGAGG AACAGGGTCA CCCACATCTT GAACATGGCC CGGGAGATTG ACAACTTCTA
1141 CCCTGAGCGC TTCACCTACC ACAATGTGCG CCTCTGGGAT GAGGAGTCGG CCCAGCTGCT
1201 GCCGCACTGG AAGGAGACGC ACCGCTTCAT TGAGGCTGCA AGAGCACAGG GCACCCACGT
1261 GCTGGTCCAC TGCAAGATGG GCGTCAGCCG CTCAGCGGCC ACAGTGCTGG CCTATGCCAT
1321 GAAGCAGTAC GAATGCAGCC TGGAGCAGGC CCTGCGCCAC GTGCAGGAGC TCCGGCCCAT
1381 CGCCCGCCCC AACCCTGGCT TCCTGCGCCA GCTGCAGATC TACCAGGGCA TCCTGACGGC
1441 CAGCCGCCAG AGCCATGTCT GGGAGCAGAA AGTGGGTGGG GTCTCCCCAG AGGAGCACCC
1501 AGCCCCCTGAA GTCTCTACAC CATTCACCAC TCTTCGCCA GAACCTGAGG GTGGTGGGA
1561 GGAGAAGGTT GTAGGCATGG AAGAGAGCCA GGCAGCCCCG AAAGAAGAGC CTGGGCCACG
1621 GCCACGTATA AACCTCCGAG GGGTCATGAG GTCCATCAGT CTTCTGGAGC CCTCCTTGGG
1681 GCTGGAGAGC ACCTCAGAGA CCAGTGACAT GCCAGAGGTC TTCTCTTCCC ACGAGTCTTC
1741 ACATGAAGAG CCTCTGAGC CCTTCCCACA GCTTGCAAGG ACCAAGGGAG GCCAGCAGGT
1801 GGACAGGGGG CCTCAGCCTG CCCTGAAGTC CCGCCAGTCA GTGGTTACCC TCCAGGGCAG
1861 TGCCGTGGTG GCCAACCGBA CCCAGGCCTT CCAGGAGCAG GAGCAGGGGC AGGGGCAGGG
1921 GCAGGGAGAG CCCTGCATTT CCTCTACGCC CAGGTTCCGG AAGGTGGTGA GACAGGCCAG
1981 CGTGCATGAC AGTGGAGAGG AGGGCGAGGC CTGAGCCCTC ACACATGCCC ACGCTCCCCCT
2041 GACACTGAAG AGGATCCACA ACTCCTTGGA GAAACACCCT CACGTCTGTT GCCGCACACA
2101 TTCCTCTCAG CTCCGCCCCA TACCGCTCAC TACAGCCTCA CCTCCCACCC CTGTCACTAC
2161 GGCCTCACCT CCCACCCCTG TCACTACAGC CTCACCTCCT ACAGCCTTAA GTCCCAGGCC
2221 CATGTCTGCC TGTTCAAGGG CTCAAGACTT TCTAACTGGG ATGTGGTAGA GGGACTGAAG
2281 GTACCTTTGG GGGCAACAGC ACCCTAGTTT CATTCTCAAC TCTAGCCCTG CACTCTACC
2341 TGTGGCACGG AATGAAAACA GAGCTTCCCG TGCAAAAAGG GTCACGCCTC CCACCCCGC
2401 CCCCTCCCTG CACCTCCTGT CCTCTCCCAG TTCATTCTG GAACCAGCCA GGCCAGGCAA
2461 CCACTGGCCC CCAAAGGCAG GCAGGATCCT CAGGCCCCAG CCGCGGGAGG CTGGAAGGGC
2521 TGGCAGATCG CTTCCTCAT CCACCTCCAC CGGTCCAGGT CTTTGCTGCT GTCCCCAGAC
2581 CTCCTGTGAC ACCACGCCAG ATCACAGGGC ACCAGGCCAG AGATAGTCTT CTTTTGTCC
2641 TTTCTGGCCT CTGGCTAGTC AGTTTTTCAT AGCCTTACAG TATCTGGCTT TGTACTGAGA
2701 AATAAAACAC ATTTTCAT

Figure 2

MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDAAEASSEPTEKAPSEELHGD
QTDFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAPRPPRLRYLLVVSTREGEGLSQDETVLLGVDFPDS
SSPSCITLGLVLPWSDTQVYLDGDDGGFSVTSGGQSRIFKPISIQTMWATLQVLHQACEAALGSGLVPGGSSALTWASH
YQERLNSEQSCLNEWTAMADLES LRPPSAEPGGSSEQEQMEQAIRAELWKVLDVSDLESVTSKEIRQALELRLGLPL
QQYRDFIDNQMLLLVAQRDRASRIFPHLYLGSEWNAANLEELQRNRVTHILNMAREIDNFYPERFTYHNVRLWDEES
AQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRSAATVLAYAMKQYECSEALRHVQELRPIARPNGFLRQLQI
YQGILTASRQSHVWEQKVGVSPEEHPAPEVSTPFPPLPPEPEGGEEKVVGMEESQAAPKEEPGPRPRINLRGVMR
SISLLEPSLELESTSETSDMPEVFSSHESSHEEPLQFPQLARTKGGQQVDRGPQPALKSRQSVVTLQGSVAVNRT
QAFQEQEQGGGGGGGEGPCISSTPRFRKVVRQASVHDSGEEGEA

Figure 3

	1	10	20	30	40	50	60	70	80	90
PYST1	1									
MKP-7										
MKP-4										
hVH5										
PAC1										
MKP-1										
MKP-2										
MKP-5										
VHR										
AK001790										
Consensus										

DGSPLSNSQSPFPVEILPFLYLGCCKDSTNLDVLEFGIKYILNVTP-----NLPNLFENAGEFKYKQIPISDHWSQNLSSQFFPERAIS
 DGSPVPSQPAFPVQILPFLYLGCCKDSTNLDVLEFGIKYILNVTP-----NLPNLFENAGEFKYKQIPISDHWSQNLSSQFFPERAIS
 ATPPPVGLRASFPVQILPFLYLGSARDSANLESALGIRYILNVTP-----NLPNLFENAGEFKYKQIPISDHWSQNLSSQFFPERAIS
 LSQCLPVPVSVGLTRILPFLYLGSQKQVNLKDLMTQNGISYVLNASH-----SCPKP-DFICESRFRHVPINDNYCEKLLPWLKSIIE
 SDPRPIYQGGPVEILPFLYLGSCHSSDLQGLQACGITAYLVNSA-----SCPNHFE---GLFHYKSIIPVEDNHKADISSHMFNEARIS
 SSCSTPLHQGGPVEILPFLYLGSAYHARRDMLDALGITALLNVSS-----NCPNHFE---GHYQYKSIIPVEDNHKADISSHMFNEARIS
 SSCSTPLHQGGPVEILPFLYLGSAYHARRDMLDALGITALLNVSS-----NCPNHFE---GHYQYKSIIPVEDNHKADISSHMFNEARIS
 NVSYRPAHQGGPVEILPFLYLGSAYHARRDMLDALGITALLNVSS-----NCPNHFE---GHYQYKSIIPVEDNHKADISSHMFNEARIS
 DSGGCYSLPSQPCNEVTPRIYVGNASVAQDIPKLGKLGITHYLNAREGRSFHMYNTNANFYKDSGITYLGIKANDTQEFNLSAYFERAAD
 -----HEGTHMHQQRPVLSQQHPFSFILNSSPAHSPHAREIDNFPY-----ERFTYHNVRMLDEESAQLLPHMKETHR
pveilp.lylgsa.....\$.....gi.....LWvs.....pn.f.....%k.p..D.....ls..f.eai..

	91	100	110	120	130	140	150	160	164
PYST1	1								
MKP-7									
MKP-4									
hVH5									
PAC1									
MKP-1									
MKP-2									
MKP-5									
VHR									
AK001790									
Consensus									

FIDEA-RGKNCGLVHCLAGISRSVTVVAYLMQKLNLSHNDAYDIYKHKKSNI SPNFMFMGQLLDFERTLGLS
 FIDEA-RSKKCGVLVHCLAGISRSVTVVAYLMQKLNLSHNDAYDIYKHKKSNI SPNFMFMGQLLDFERTLGLS
 FIDEA-LSQKCGVLVHCLAGISRSVTVVAYLMQKLNLSHNDAYDIYKHKKSNI SPNFMFMGQLLDFERTLGLS
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 FIDSV-KNSGGRVTVHCLAGISRSATIAIAYIMKTGHSDDAYRFVKDRRPSISPNFNLGQLLEYERTLKL
 FIDSI-KNAGGRVTVHCLAGISRSATIAIAYIMKTGHSDDAYRFVKDRRPSISPNFNLGQLLEYERTLKL
 YIDAV-KDCRGRVTVHCLAGISRSATIAIAYIMKTGHSDDAYRFVKDRRPSISPNFNLGQLLEYERTLKL
 YIDCV-KDCRGRVTVHCLAGISRSATIAIAYIMKTGHSDDAYRFVKDRRPSISPNFNLGQLLEYERTLKL
 FIDCV-REKGGKVLVHCLAGISRSATIAIAYIMKTGHSDDAYRFVKDRRPSISPNFNLGQLLEYERTLKL
 FIDQALAQKNGRVLVHCLAGISRSATIAIAYIMKTGHSDDAYRFVKDRRPSISPNFNLGQLLEYERTLKL
 FIEAA-RAQGTHTVLVHCLAGISRSATIAIAYIMKTGHSDDAYRFVKDRRPSISPNFNLGQLLEYERTLKL
 FI#.a.....VIVHC.agISRSat....AYIM.....sl..a.....ik.r..isPNF.F\$gQLL...l...l...

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Figure 4

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1  CCGGTGCCAG CCCAGGTGCT CGCGGCCTGG CTCCATGGCC CTGGTCACAG TGAGCCGTTC
61  GGGGGCCCTGG GGGGGCCCTGG GGGGGCCCTGG GGGGGCCCTGG GGGGGCCCTGG
121 GAGTCGACTC CAGCGAAGGC AGAGCTTTGC GGTGCTCCGT GGGGGCTGTCC TGGGACTGCA
181 GGATGGAGGG GACAATGATG ATGCAGCAGA GGCCAGTTCT GAGCCAACAG AGAAGGCCCC
241 GAGTGAGGAG GAGCTCCACG GGGACCAGAC AGACTTCGGG CAAGGATCCC AGAGTCCCCA
301 GAAGCAGGAG GAGCAGAGGC AGCACCTGCA CCTCATGGTA CAGCTGCTGA GGCCGCAGGA
361 TGACATCCGC CTGGCAGCCC AGCTGGAGGC ACCCGGCCCT CCCC GGCTCC GCTACCTGCT
421 GGTAGTTTCT ACACGAGAAG GAGAAGGTCT GAGCCAGGAT GAGACGGTCC TCCTGGGCGT
481 GGATTTCCCT GACAGCAGCT CCCCAGCTG CACCCTGGGC CTGGTCTTGC CCCTCTGGAG
541 TGACACCCAG GTGTACTTAG ATGGAGACGG GGGCTTCAGC GTGACGTCTG GTGGGCAAAG
601 CCGGATCTTC AAGCCCATCT CCATCCAGAC CATGTGGGCC AACTCCAGG TATTGCACCA
661 AGCATGTGAG GCAGCTCTAG GCAGCGGCCT TGTACGGGT GGCAGTGCCC TCACCTGGGC
721 CAGCCACTAC CAGGAGAGAC TGAAGTCCGA ACAGAGCTGC CTCAATGAGT GGACGGCTAT
781 GGCCGACCTG GAGTCTCTGC GGCTCCCGAG CGCCGAGCCT GGCGGGTCCT CAGAACAGGA
841 GCAGATGGAG CAGGCGATCC GTGCTGAGCT GTGGAAAGTG TTGGATGTCA GTGACCTGGA
901 GAGTGTCACT TCAAAGAGA TCCGCCAGGC TCTGGAGCTG CGCCTGGGGC TCCCCCTCCA
961 GCAGTACCGT GACTTCATCG ACAACCAGAT GCTGCTGCTG GTGGCACAGC GGGACCGAGC
1021 CTCCCGCATC TTCCCCACC TCTACCTGGG CTCAGAGTGG AACGCAGCAA ACCTGGAGGA
1081 GCTGCAGAGG AACAGGGTCA CCCACATCTT GAACATGGCC CGGGAGATTG ACAACTTCTA
1141 CCTGAGCGC TTCACCTACC ACAATGTGCG CCTCTGGGAT GAGGAGTCGG CCCAGCTGCT
1201 GCCGCACTGG AAGGAGACGC ACCGCTTCAT TGAGGCTGCA AGAGCACAGG GCACCCACGT
1261 GCTGGTCCAC TGCAAGATGG GCGTCAGCCG CTCAGCGGCC ACAGTGCTGG CCTATGCCAT
1321 GAAGCAGTAC GAATGCAGCC TGGAGCAGGC CCTGCGCCAC GTGCAGGAGC TCCGGCCCAT
1381 CGCCGCCCC AACCCTGGCT TCCTGCGCCA GCTGCAGATC TACCAGGGCA TCCTGACGGC
1441 CAGAACCTGA GGGTGGTGGG GAGGAGAAGG TTGTAGGCAT GGAAGAGAGC CAGGCAGCCC
1501 CGAAAGAAGA GCCTGGGCCA CGGCCACGTA TAAACCTCCG AGGGGTCTATG AGGTCCATCA
1561 GTCTTCTGGA GCCCTCCTTG GAGCTGGAGA GCACCTCAGA GACCAGTGAC ATGCCAGAGG
1621 TCTTCTCTTC CCACGAGTCT TCACATGAAG AGCCTCTGCA GCCCTTCCCA CAGCTTGCAA
1681 GGACCAAGGG AGGCCAGCAG GTGGACAGGG GGCCCTCAGC TGCCCTGAAG TCCCGCCAGT
1741 CAGTGGTTAC CCTCCAGGGC AGTGCCGTGG TGGCCAACCG GACCCAGGCC TTCCAGGAGC
1801 AGGAGCAGGG GCAGGGGCAG GGGCAGGGAG AGCCCTGCAT TTCCTCTACG CCCAGGTTCC
1861 GGAAGGTGGT GAGACAGGCC AGCGTGCATG ACAGTGGAGA GGAGGGCGAG GCCTGAGCCC
1921 TCACACATGC CCACGCTCCC CTGACACTGA AGAGGATCCA CAACTCCTTG GAGAAACACC
1981 CTCACGTCTG TTGCCGACA CATTCCCTCT AGCTCCGCC CATAACCGTC ACTACAGCCT
2041 CACCTCCCAC CCCTGTCACT ACGGCCTCAC CTCCCACCCC TGTCACTACA GCCTCACCTC
2101 CTACAGCCTT AAGTCCCAGG CCCATGTCTG CCTGTCCAAG GGCTCAAGAC TTTCTAACTG
2161 GGATGTGGTA GAGGGACTGA AGGTACCTTT GGGGGCAACA GCACCCTAGT TTCAATTCTCA
2221 ACTCTAGCCC TGCACACTCA CCTGTGGCAC GGAATGAAAA CAGAGCTTCC CGTGCAAAAA
2281 GGGTCACGCC TCCCACCCCC GCCCCCTCCC TGCACCTCCT GTCCTCTCCC AGTTCATTCC
2341 TGGAACCCAGC CAGGCCAGGC AACCAGTGGC CCCC AAAGGC AGGCAGGATC CTCAGGCCCC
2401 AGCCGCGGGA GGCTGGAAGG GCTGGCAGAT CGCTTCCCTC ATCCACCTCC ACCGGTCCAG
2461 GTCTTTGCTG CTGTCCCCAG ACCTCCTGTG ACACCACGCC AGATCACAGG GCACCAAGCC
2521 AGAGATAGTC TTCTTTTGT CTTTCTGGC CTCTGGCTAG TCAGTTTTTC ATAGCCTTAC
2581 AGTATCTGGC TTTGTACTGA GAAATAAAAC ACATTTTC

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Figure 5

MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFVAVLRGAVLGLQDGGDNDDAAEASSEPTEKAPSEELHGD
QTDGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAPRPPRLRYLLVVSTREGEGLSQDETULLGVDFPDS
SSPCTLGLVLPLWSDTQVYLDGGGFSVTSGGQSRIFKPISIQTMWATLQVLHQACEAALGSGLVPGGSALTWASH
YQERLNSEQSCLNEWTAMADLESRLPPSAEPGGSSEQEQMEQAIRAELWKVLDVSDLESVTSKEIRQALELRLGLPL
QQYRDFIDNQMLLLVAQRDRASRIFPHLYLGSEWNAANLEELQRNRVTHILNMAREIDNFYPERFITYHNVRWDEES
AQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRSAATVLAYAMKQYECSSLEQALRHVQELRPIARPNGFLRQLQI
YQGILTART

213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300
213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300